

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 29, 2003, 15:09:02 ; Search time 22 Seconds

(without alignments)
152.708 Million cell updates/sec

Title: US-09-924-102-2

Perfect score: 418

1 MLLSHLFLVLFIVLPSYL..... RWGGGGGRGGTADTGGMFLS 81

Scoring table: Biosum62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. 1s is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	68	16.3	462	SR54_HAETN
2	68	16.3	511	COPD_HUMAN
3	67	16.0	829	TOP1_XENLA
4	65	15.6	829	RPR_DROME
5	65	15.6	386	RRSL_HUMAN
6	64	15.4	365	COPD_BOVIN
7	64	15.3	511	TOP1_HUMAN
8	64	15.3	765	TOP1_MOUSE
9	64	15.3	767	DNAJ_HALCU
10	63.5	15.2	391	DNAQ_HALMU
11	63.5	15.2	1	TRHY_HUMAN
12	62	14.8	1898	EP34_HCMVA
13	61.5	14.7	259	RS2_CAEEL
14	61.5	14.7	272	EP84_HCMVA
15	61.5	14.7	684	ROU_HUMAN
16	61	14.6	824	DMSL_PHYBL
17	61	14.6	78	LA_BOVIN
18	61	14.6	404	DNAE_HELIC
19	61	14.6	486	TOP1_CRICK
20	61	14.6	767	SYA_SALTI
21	61	14.6	876	SIA_SALTY
22	61	14.6	876	LEL3_GOSH
23	59.5	14.2	165	THC1_METTH
24	59.5	14.2	433	EVA_DROME
25	59.5	14.2	766	OBZ445_salmoneilla
26	59	14.1	307	OBZ446_salmoneilla
27	59	14.1	519	OBZ447_drosophila
28	59	14.1	524	OBZ448_xenopus
29	59	14.1	739	OBZ449_pseudomas
30	59	14.1	1029	OBZ450_rhizobium_m
31	58.5	14.0	1	OBZ451_haloferaci
32	58.5	14.0	365	OBZ452_musculu
33	58.5	14.0	1228	OBZ453_homo_sapien

RESULT 1

ID	SR54_HAETN	STANDARD;	PRT;	462 AA.
SR54_HAETN				
ID				
AC				
PA4518;				
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Signal recognition particle protein (Fifty-four homolog).			
GN	FFH OR H10106.			
RA	Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips T.A., Spirogs T., Heblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Fuhrmann J.L., Geoghegan N.S.M., McDonald C.L., McDonald T.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;			
RA	"Whole genome random sequencing and assembly of Haemophilus influenzae Rd.";			
RA	Science 269:496-512(1995).			
RL	- FUNCTION: NECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM THE RIBOSOMES (BY SIMILARITY).			
CC	- SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECULE AND PROTEIN FFH (BY SIMILARITY).			
CC	- DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGNAL SEQUENCE.			
CC	- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.			
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CC	EMBL; U32696; AAC21784.1; -.			
DR	TIGR; H10106; -.			
DR	InterPro; IPR03593; AAA_ATPase.			
DR	InterPro; IPR000597; SRP54.			
DR	InterPro; IPR04125; SRP54_SPB.			
DR	InterPro; IPR04780; SRP_sub.			
DR	PFam; PF00448; SRP54; 1.			
DR	Pfam; PF02881; SRP54_N; 1.			

ALIGNMENTS

DR	Pfam; PRO22978; SRP_SPB; 1;
DR	ProDom; RD000813; SRP5; 1;
DR	TIGRFAMS; TIGR00959; 3a0501s01; 1;
DR	SMART; SM0382; AAA; 1;
KW	signal recognition particle; GTP-binding; RNA-binding;
KW	Complete proteome.
FT	DOMAIN 1 295 G-DOMAIN.
FT	DOMAIN 296 453 M-DOMAIN.
FT	NP_BIND 107 114 GTP (BY SIMILARITY).
FT	NP_BIND 190 194 GTP (BY SIMILARITY).
FT	NP_BIND 248 251 GTP (BY SIMILARITY).
SQ	SEQUENCE 462 AA; 50843 MW; 164C32099A15BP7A CRC64;
RESULT 2	Query Match 16.3%; Score 68; DB 1; Length 462; Best Local Similarity 27.9%; Pred. No. 3.7; Matches 29; Conservative 14; Mismatches 31; Indels 30; Gaps 5;
ID	COPD_HUMAN
STANDARD	PRT; 511 AA.
AC	P48444;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, last sequence update)
DE	Coatomer delta subunit (Delta-coat protein) (Delta-COP) (Archain).
GN	COPD OR ARCN1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TAXID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE:95301274; PubMed=7782067;
RA	Radicci P., Pensotti V., Jones C., Perry H., Pierotti M.A., Tunnicliffe A.;
RT	"The human archain gene, ARCN1, has highly conserved homologs in rice and Drosophila.", Genomics 26:101-106(1995).
CC	-1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC PROTEIN TRANSPORT FROM THE ER VIA THE GOLGI UP TO THE TRANS GOLGI NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDGING FROM GOLGI MEMBRANES, AND IS ESSENTIAL FOR THE RETROGRADE GOLGI-TO-ER TRANSPORT OF DILYSINE-TAGGED PROTEINS. IN MAMMALS, THE COATOMER CAN ONLY BE RECRUITED BY MEMBRANES ASSOCIATED TO ADP-RIBOSYLATION FACTORS (ARFs), WHICH ARE SMALL GTP-BINDING PROTEINS; THE COMPLEX ALSO INFLUENCES THE GOLGI STRUCTURAL INTEGRITY, AS WELL AS THE PROCESSING, ACTIVITY, AND ENDOCYTIC RECYCLING OF LDL RECEPTORS (BY SIMILARITY).
CC	-1- SUBUNIT: OLIGOMERIC COMPLEX THAT CONSISTS OF AT LEAST THE ALPHA, BETA, BETA', GAMMA, DELTA, EPSILON AND ZETA SUBUNITS. THE COMPLEX IS SUBCELLULAR LOCATION: THE COMOMER IS CYTOSLAMIC OR POLYMERIZED ON THE COTYPOPLASMIC SIDE OF THE GOLGI, AS WELL AS ON THE VESICLES/ENDS ORIGINATING FROM IT (BY SIMILARITY).
CC	-1- TISSUE SPECIFICITY: UBIQUITINOSLY EXPRESSED.
CC	-1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS FAMILY. COPD SUBFAMILY.
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RESULT 3	Query Match 16.3%; Score 68; DB 1; Length 511; Best Local Similarity 21.1%; Pred. No. 4.1; Matches 20; Conservative 24; Mismatches 29; Indels 22; Gaps 2;
ID	TOP1_XENLA
STANDARD	PRT; 57210 MW; 4ED1F7D2D12A7F75 CRC64;
AC	P41512;
DT	01-NOV-1995 (Rel. 32, Created)
DE	Coatomer delta subunit (Delta-coat protein) (Archain).
GN	TOP1
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.
OX	NCBI_TAXID=8355;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE:96433160; PubMed=8836188;
RA	Pandit S.D., Richard R.E., Sternglanz R., Bogenhagen D.F.; Cloning and characterization of the gene for the somatic form of DNA topoisomerase I from Xenopus laevis., Nucleic Acids Res. 24:3593-3600(1996).
RT	-1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER. CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.
CC	-1- SUBUNIT: MONOMER.
CC	-1- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.
CC	-1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
CC	-1- SIMILARITY: BELONGS TO THE EUKARYOTIC TYPE I TOPOISOMERASE FAMILY.
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RT "Characterization of the major hnRNP proteins from Drosophila
 RT melanogaster";
 RL Cell Biol. 116:257-269(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S; TISSUE=Embryo;
 RX MEDLINE=92020124; PubMed=1717937;
 RA Hovemann B.T., Dessen E., Mechler H., Mack E.;
 RT "Drosophila snRNP associated protein p11 which specifically binds to
 heat shock puff 93D reveals strong homology with hnRNP core protein
 R1 heat.";
 Nucleic Acids Res. 19:4909-4914(1991).
 -1- FUNCTION: THIS PROTEIN IS A COMPONENT OF RIBONUCLEOSOMES. COULD BE
 NEEDED TO ORGANIZE A CONCENTRATION GRADIENT OF A DORSALIZING
 MORPHOGEN (DM) ORIGINATING IN THE GERMINAL VESICLE.
 -1- SUBCELLULAR LOCATION: NUCLEAR AND/OR CYTOPLASMIC.
 -1- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (REM).
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 CC
 DR EMBL: X54803; CAA8574_1;
 DR EMBL: X62036; CAA4502_1; -;
 DR EMBL: X58691; CAA42212_1; -;
 DR HSSP: P09651; IUP1;
 DR Flybase: FBgn0004237; Hdb78F;
 DR InterPro: IPR000504; RNA_rec_mot;
 DR Pfam: PF0076; rrm; 2;
 DR SMART: S00060; RRM; 2;
 DR PROSITE: PS50102; RRM; 2;
 DR PROSITE: PS00030; RRM_RNP_1; 2;
 DR RNA-binding, Nuclear protein; Ribonucleoprotein; Repeat;
 KW Alternative splicing.
 FT DOMAIN 24 101 RNA-BINDING (RRM) 1.
 FT DOMAIN 115 192 RNA-BINDING (RRM) 2.
 FT VARSPLC 315 374 MISSING (IN ISOFORM HRP36.1).
 FT CONFLICT 271 271 S -> T (IN REF. 3).
 SQ SEQUENCE 386 AA; 39557 MW; 2035C0AD0E3AF7 CRC64;
 Query Match 15.6%; Score 65; DB 1; Length 386;
 Best Local Similarity 50.0%; Pred. No. 6.5; Indels 8; Mismatches 2; Gaps 1;
 Matches 13; Conservative 3; Mismatches 8; Indels 2; Gaps 1;

QY 54 RKTGKGRWGGQSGRGAGTGGM 79
 Db 231 RONG--GGNGGAGGGGGFGNNGNE 254

RESULT 6
 RRSL_HUMAN STANDARD; PRT; 365 AA.

AC 01050; Q9BU8; 36' (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribosome biogenesis regulatory protein homolog.
 GN RRS1_HUMAN
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97011152; PubMed=8958162;
 RA Faustich D., Auerbach S., Orci L., Ravazzola M., Wegehingel S.,
 RA Loeffstreich F., Stenbeck G., Harter C., Wieland F.T., Tschochner H.;
 RT "Architecture of coatomer: molecular characterization of delta-COP
 and protein interactions within the complex.";
 RT J. Cell Biol. 135:53-61(1998).
 CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
 TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
 CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
 CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
 CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI

RT the coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
 RT analysis of cDNA clones from human cell line KG-1.";
 RL DNA Res. 2:37-43(1995).
 RN [21]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, and Uterus;
 RA Strasbourg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SUBCELLULAR LOCATION:
 RA Scherf A., Couet Y., Decon C., Sanchez J.-C., Diaz J.-J.,
 RA Hochstrasser D.;
 RT "Proteomic analysis of the nucleus.";
 RL (In) Palagi P.M., Sanchez J.-C., Stoicklin R. (eds.);
 Proceedings of the Swiss Proteome Society, 2001 Congress Functional
 Proteomics, pp.124-124, Fontis Media, Lausanne (2001).
 CC -1- FUNCTION: Involved in ribosome biogenesis (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear; nucleolar.
 CC -1- SIMILARITY: BELONGS TO THE RRS1 FAMILY.
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 CC
 DR EMBL: D05218; BAA04948_1; ALT_INIT.
 DR EMBL; BC00181; ARH0181_1; -.
 DR SWISS-2DPAGE: 015050; HUMAN.
 KW Ribosome biogenesis; Nuclear protein.
 FT DOMAIN 302 365 ARG/GLY/LYS-RICH.
 SQ SEQUENCE 365 AA; 41193 MW; 061C3A6174C2E7C2 CRC64;
 Query Match 15.4%; Score 64.5; DB 1; Length 365;
 Best Local Similarity 37.5%; Pred. No. 6.9;
 Matches 18; Conservative 6; Mismatches 17; Indels 7; Gaps 2;
 QY 29 RKTGKGRWGGQSGRGAGTGGM 76
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coatomer delta subunit (Delta-coat protein) (Delta-COP).
 GN COPD.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovine; Bos.
 OX NCBI_TaxID=9913;
 RN [1] SEQUENCE OF 2-511 FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=97011152; PubMed=8958162;
 RA Faustich D., Auerbach S., Orci L., Ravazzola M., Wegehingel S.,
 RA Loeffstreich F., Stenbeck G., Harter C., Wieland F.T., Tschochner H.;
 RT "Architecture of coatomer: molecular characterization of delta-COP
 and protein interactions within the complex.";
 RT J. Cell Biol. 135:53-61(1998).
 CC -1- FUNCTION: THE COATOMER IS A CYTOSOLIC PROTEIN COMPLEX THAT BINDS
 TO DILYSINE MOTIFS AND REVERSIBLY ASSOCIATES WITH GOLGI NON-
 CLATHRIN-COATED VESICLES, WHICH FURTHER MEDIATE BIOSYNTHETIC
 CC PROTEIN TRANSPORT FROM THE ER, VIA THE GOLGI UP TO THE TRANS GOLGI
 CC NETWORK. COATOMER COMPLEX IS REQUIRED FOR BUDDING FROM GOLGI

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DR EMBL; J03250; AAA61207_1; -.

DR EMBL; M60705; AAA61206_1; JOINED.

DR EMBL; M60688; AAA61206_1; JOINED.

DR EMBL; M60689; AAA61206_1; JOINED.

DR EMBL; M60690; AAA61205_1; JOINED.

DR EMBL; M60691; AAA61206_1; JOINED.

DR EMBL; M60692; AAA61206_1; JOINED.

DR EMBL; M60693; AAA61205_1; JOINED.

DR EMBL; M60694; AAA61206_1; JOINED.

DR EMBL; M60695; AAA61206_1; JOINED.

DR EMBL; M60696; AAA61206_1; JOINED.

DR EMBL; M60697; AAA61205_1; JOINED.

DR EMBL; M60698; AAA61206_1; JOINED.

DR EMBL; M60699; AAA61206_1; JOINED.

DR EMBL; M60700; AAA61206_1; JOINED.

DR EMBL; M60701; AAA61206_1; JOINED.

DR EMBL; M60702; AAA61206_1; JOINED.

DR EMBL; M60703; AAA61205_1; JOINED.

DR EMBL; M60704; AAA61206_1; JOINED.

DR EMBL; M60705; AAA61205_1; JOINED.

DR EMBL; U07804; AAA60309_1; -.

DR EMBL; U07806; AAA60308_1; -.

DR EMBL; AL035652; CAB43980_1; -.

DR EMBL; X16479; CAR34500_1; ALT_INIT.

DR EMBL; M27913; AAA61208_1; -.

DR PIR; A30887; ISHUT1.

DR PDB; I331; 19-AUG-98.

DR PDB; I335; 26-AUG-98.

DR PDB; I336; 12-AUG-98.

DR Harnisch/Ghent-2DPAGE; 610; NEPHGE.

DR HGNC; 111986; TOP1.

DR MIM; 126420; -.

DR InterPro; IPR01631; Topoisomerase_I.

DR Pfam; PF01028; Topoisomerase_I; 1.

DR Pfam; PF02919; topoisomerase_I_N; 1.

DR PRINTS; PRO0416; EUTPISMSREI.

DR SMART; SM00435; TOPEUC; 1.

DR PROSITE; PS00176; TOPoisomerase_I_EUK; 1.

KW Isoenzyme; Topoisomerase; DNA-binding; Polymorphism; 3D-structure.

FT DOMAIN 191 197 POLY-LYS

FT ACT-SITE 723 723 DNA CLEAVAGE (BY SIMILARITY)

FT VARIANT 370 370 M -> T (IN CPT-RESISTANT CELL LINE)

FT /FTID=VAR_010666

FT D -> G (IN CPT-RESISTANT CELL).

FT /FTID=VAR_007531

FT N -> S (IN CPT-RESISTANT CELL LINE)

FT CEM/C2).

FT /FTID=VAR_010667

FT T -> A (IN CPT-RESISTANT CELL).

FT ACT-SITE 725 725 DNA CLEAVAGE (BY SIMILARITY).

FT CONFLICT 145 145 A -> V (IN REF. 1).

FT SEQUENCE 765 AA; 90725 MW; 6FBED540BCF7BE28 CRC64;

Query Match 15.3%; Score 64; DB 1; Length 767;

Best Local Similarity 30.0%; Pred. No. 17; Matches 18; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 18 YSLGDRARLCLRKTKQQKEQQILRQSEVLFASETLRKGKGRGGTADTGG 77

Dy 444 YETARRKKVDKDVKIRNQYREDWKSKEMKVQRQAVALYFIDKLALRAGNEKEGETADPG 503

RESULT 9

TOP1_MOUSE	STANDARD	PRT	767 AA.
ID_TOPI_MOUSE			004750; 01-OCT-1993 (Rel. 27, Created)

DR NCBI_TaxId=10090; OX Mus musculus (Mouse); OC Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus. RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=33216125; PubMed=809688;

RA Koivai O., Yasui Y., Sakai Y., Watanabe T., Ishii K., RA Yangihara S., Andoh T.; RT Cloning of the mouse cDNA encoding DNA topoisomerase I and chromosomal location of the gene.; Gene 125:211-216(1993). [2]

RN SEQUENCE FROM N.A.

RA Hui C.F., Lo C.K., Hwang J.; RT Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.

CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

CC -1- CATALYTIC ACTIVITY: AMP-Independent breakage of single-stranded DNA, followed by passage and rejoining.

CC -1- SUBUNIT: MONOMER.

CC -1- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND IT CAN RELAX BOTH NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.

CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC TYPE I TOPOISOMERASE FAMILY.

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DR EMBL; D10061; BAA00950_1; -.

DR EMBL; L20632; AAA40466_1; -.

DR PIR; JU0144; JU0144.

DR HSSP; P1137; I35.

DR MGD; MG1:98778; TOP1.

DR InterPro; IPR01631; Topoisomerase_I.

DR Pfam; PF01028; Topoisomerase_I; 1.

DR PRINTS; PRO0416; EUTPISMSREI.

DR SMART; SM00435; TOPEUC; 1.

DR PROSITE; PS00176; TOPoisomerase_I_EUK; 1.

KW Isomerase; Topoisomerase; DNA-binding.

FT ACT-SITE 725 725 DNA CLEAVAGE (BY SIMILARITY).

FT CONFLICT 91 91 R -> P (IN REF. 2).

FT CONFLICT 121 121 D -> E (IN REF. 2).

FT CONFLICT 129 129 A -> V (IN REF. 2).

FT CONFLICT 161 161 MISSING (IN REF. 2).

FT CONFLICT 167 167 S -> L (IN REF. 2).

FT CONFLICT 277 277 R -> W (IN REF. 2).

FT CONFLICT 292 292 G -> E (IN REF. 2).

FT CONFLICT 522 522 G -> V (IN REF. 2).

FT CONFLICT 533 533 G -> W (IN REF. 2).

FT CONFLICT 762 762 D -> Y (IN REF. 2).

SQ SEQUENCE 767 AA; 90769 MW; 398327062B179P2A CRC64;

Query Match 15.3%; Score 64; DB 1; Length 767;

Best Local Similarity 30.0%; Pred. No. 17; Matches 18; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

QY 18 YSLGDRARLCLRKTKQQKEQQILRQSEVLFASETLRKGKGRGGTADTGG 77

Db 446 VETARRKKVCDKIRNQYREDWKSKEMKVRORAVALLYFIDKLALRAGNEKEGETADTVG 505

Best Local Similarity 32.7%; Pred. No. 9.5

RESULT 10
DNAJ_HALCU

Qy Best Local Similarity 32.4%; Pred. No. 9.5;
Matches 18; Conservative 5; Mismatches 27; Indels 5; Gaps 1;
30 KTKQQKEQQIL---ROSEVLERSETLRKGKRRWMGCGGGGTADTGGMF 79
| : || : || | | : | : | | | | | | | | | | | | | | | | | | | |

RESULT	11			
ID	DNAJ_HALN1	STANDARD;	PRT;	391 AA.
AC	O9HRY3;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Chaperone protein dnaJ.			
GN	DNAJ OR VNG0489G			
OS	Halobacterium sp. (strain NRC-1).			
OC	Archaea; Euryarchaeota; Halobacteria; Halobacterales;			
OX	Halobacteriaceae; Halobacterium.			
RN	NCBI_TAXID=64091;			
RP	[1]			
SEQUENCE FROM N.A.				
RX	MEDLINE=20304483; PUBMED=11016950;			
RA	Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Ballina N.S., Thorsson V., Sbragna J., Swartrell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenberger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Daniels C.J., Dennis P.R., Omer A.D., Edhardt H., Lowe T.M., Liang P., Riley M., Hood L., Bassarma S.; RT "Genome sequence of Halobacterium species NRC-1.";			
RL	Proc. Natl. Acad. Sci. U. S. A. 97:12176-12181 (2000)			
CC	-I- FUNCTION: ACTS AS A CO-CHAPERONE. SIMULATES, JOINTLY WITH GRPE, THE ATPASE ACTIVITY OF DNAK (BY SIMILARITY).			
CC	-I- COFACTOR: BINDS TWO ZINC IONS PER MONOMER (BY SIMILARITY).			
CC	-I- SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).			
CC	-I- SIMILARITY: BELONGS TO THE DNAJ FAMILY.			
CC	-I- SIMILARITY: CONTAINS 1 J DOMAIN.			
CC	-I- SIMILARITY: CONTAINS 1 CR DOMAIN.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@ib-sib.ch).			
CC	EMBL; AE005002; AAG19025; 1; - .			
DR	HSSP; P08622; IBO2.			
DR	InterPro; IPR02939; DnaJ_C.			
DR	InterPro; IPR01305; DnaJ_LCXXCGXG.			
DR	InterPro; IPR01623; DnaJ_N.			
DR	InterPro; IPR03095; Hsp_DnaJ.			
DR	Pfam; PF00226; DnaJ; 1.			
DR	Pfam; PF00684; DnaJ_CGXCGXG; 1.			
DR	Pfam; PF01556; DnaJ_C; 1.			
DR	PRINTS; PRO0625; DNAJPROTEIN.			
DR	SMART; SM00271; DnaJ_1.			
DR	PROSITE; PS00636; DNAJ_1; FALSE_NEG.			
DR	PROSITE; PS00076; DNAJ_2; 1.			
DR	PROSITE; PS00637; DNAJ_CXXCGXG; FALSE_NEG.			
KW	Chaperone; DNA replication; Heat shock; Repeat; zinc; Metal-binding; Complete proteome.			
FT	DOMAIN 4 68 J-DOMAIN.			
FT	DOMAIN 79 131 GLY-RICH.			
FT	REPEAT 165 172 CXXCGXG MOTIF.			
FT	REPEAT 182 189 CXXCGXG MOTIF.			
FT	REPEAT 203 215 CXXCGXG MOTIF.			
FT	REPEAT 222 229 CXXCGXG MOTIF.			
FT	METAL 165 165 ZINC 1 (BY SIMILARITY).			

RESULT 13

EP34_HCMVA STANDARD; PRT; 268 AA.

ID EP34_HCMVA STANDARD; PRT; 268 AA.

AC P16768; CC

DT 01-FEB-1990 (Rel. 15, Created) CC

DT 30-MAY-2000 (Rel. 30, Last annotation update) CC

DE Early phosphoprotein P34. CC

GN UL12. CC

OS Human cytomegalovirus (strain AD169). CC

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; CC

OC Betaherpesvirinae; Cytomegalovirus. CC

OX NCBI_TaxID=10360; CC

RN [1] SEQUENCE FROM N.A. CC

RP MEDLINE=90269039; PubMed=2161319; DR

RX Chee M.S., Banquier A.T., Beck S., Bohni R., Brown C.M., Cerny R., DR

RA Horschell T., Hutchison C.A., III, Kouzarides T., Martignetti J.A., DR

RA Preddle E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; DR

RT "Analysis of the protein-coding content of the sequence of human DR

RT cytomegalovirus strain AD169"; RT

Curr. Top. Microbiol. Immunol. 154:125-169(1990). DR

RN [2] SEQUENCE FROM N.A. DR

RN Wang S.K., Duh C.Y.; DR

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases. DR

CC -1 SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-6 AND DR

CC HSV-7, U79 AND HCMV UL12 (P34). DR

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or send an email to license@isb-sib.ch). DR

CC EMBL; U42436; AAF9899.1; DR

DR HSSP; P02357; 1PKP. DR

DR Wormpep; C49HB.11; CE04237. DR

DR InterPro; IPR000851; Ribosomal_S5. DR

DR Pfam; PF00333; Ribosomal_S5; 1. DR

DR Pfam; PF03719; Ribosomal_S5_C; 1. DR

DR TIGRFAMS; TIGR01020; rps2_arch; 1. DR

DR PROSITE; PS00855; RIBOSMAL_S5; 1. DR

KW Ribosomal protein; Repeat. KW

SQ SEQUENCE 272 AA; 2890 MW; 60049F5B7DB8CB34 CRC64; SQ

Query Match Wang S.K., Duh C.Y.; DR

Best Local Similarity 56.0%; DR

Matches 14; Conservative 2; DR

Mismatches 8; Indels 1; DR

Gaps 1; DR

Db 27 RPAGGRGGRRGRRGRRGAGRG 51 DR

RESULT 15

EP84_HCMVA STANDARD; PRT; 684 AA.

ID EP84_HCMVA STANDARD; PRT; 684 AA.

AC P1751; P87889; OI2567; DR

DR 01-AUG-1990 (Rel. 15, Created) DR

DT 30-MAY-2000 (Rel. 39, Last sequence update) DR

DT 30-MAY-2000 (Rel. 39, Last annotation update) DR

DE Early phosphoprotein P84. DR

GN UL112/UL113. DR

OS Human cytomegalovirus (strain AD169). DR

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; DR

OC Betaherpesvirinae; Cytomegalovirus. DR

OX NCBI_TaxID=10360; DR

RN [1] SEQUENCE FROM N.A. DR

RP MEDLINE=90269039; PubMed=2161319; DR

RX Chee M.S., Banquier A.T., Beck S., Bohni R., Brown C.M., Cerny R., DR

RA Horschell T., Hutchison C.A., III, Kouzarides T., Martignetti J.A., DR

RA Preddle E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.; DR

RT "Analysis of the protein-coding content of the sequence of human DR

RT cytomegalovirus strain AD169"; RT

Curr. Top. Microbiol. Immunol. 154:125-169(1990). DR

RN [2] REVISIONS, AND IDENTIFICATION. DR

RN Wang S.K., Duh C.Y.; DR

RP SEQUENCE FROM N.A. DR

RX Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases. DR

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or send an email to license@isb-sib.ch). DR

CC EMBL; U17403; CAA53515.1; DR

DR EMBL; U5743; AAB53251.1; DR

PIR; S09880; S09880. DR

InterPro; IPRO04138; U79_P34. DR

RESULT 14

RS2_CAEEL STANDARD; PRT; 272 AA.

ID RS2_CAEEL STANDARD; PRT; 272 AA.

AC P51403; CC

DT 01-OCT-1996 (Rel. 34, Created) CC

DT 01-OCT-1996 (Rel. 34, Last sequence update) CC

DT 15-TUN-2002 (Rel. 41, Last annotation update) CC

DE 40S ribosomal protein S2. CC

OS RPS-2 OR C49H8.11. CC

GS Caenorhabditis elegans. CC

OC Eukaryota; Metazoa; Nematoidea; Rhabditida; Rhabditoidae; CC

OC Rhabditidae; Peloderrinae; Caenorhabditis. CC

OX NCBI_TaxID=6239; CC

RN [1] SEQUENCE FROM N.A. CC

DR Pfam: PF03064: U79_P34; 1.
KW Early protein phosphorylation.
FT DOMAIN 148 153 POLY-GLY.
FT DOMAIN 197 200 POLY-SER.
FT DOMAIN 202 220 POLY-GLY.
FT DOMAIN 271 276 POLY-GLY.
FT DOMAIN 285 296 POLY-GLY.
FT DOMAIN 314 318 POLY-SER.
FT DOMAIN 321 324 POLY-SER.
FT DOMAIN 327 334 POLY-HIS.
FT DOMAIN 390 397 POLY-ALA.
FT DOMAIN 563 568 POLY-ALA.
FT DOMAIN 569 576 POLY-SER.
FT DOMAIN 578 585 POLY-PRO.
FT DOMAIN 599 606 POLY-GLY.
FT DOMAIN 615 621 POLY-SER.
SQ SEQUENCE 684 AA; 70272 MW; . F3325C2E29EF449 CRC64;

Query Match 14.7%; Score 61.5; DB 1; Length 684;
Best Local Similarity 40.5%; Pred. No 29;
Matches 17; Conservative 2; Mismatches 20; Indels 3; Gaps 1;

QY 35 KEQQILRQEVLFSETIRKTKGKGRMGQQGRGGTANGG 77
Db 179 EEQQRRRQSQ--RHEERRRKSSSSAGGGGGGGGGGGGG 217

Search completed: May 29, 2003, 15:18:41
Job time : 24 secs